

1 CAGTGTGCTG GCGGCCGGC GCGAGCCGGC CGGGCCCCGG TCGGGCCCTCC
-26

GAAACC ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC
M N F L L S W V H W S
-26 -20

90 CTC GCC TTG CTG CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG
-15 L A L L Y L H H A K W S Q
-10

GCT GCA CCC ATG CCA GAA GGA GGA GGG CAG AAT CAT CAC
A A P M A E G G G Q N H H
-1 +1 → +5 +10

171 GAA GTG GTG AAG TTC ATG GAT GTC TAT CAG CGC AGC TAC TGC
13 E V V K F M D V Y Q R S Y C
+15 +20 +25

CAT CCA ATC GAG ACC CTG GTG GAC ATC TTC CAG GAG TAC
H P I E T L V D I F Q E Y
+30 +35

252 CCT GAT GAG ATC GAG TAC ATC TTC AAG CCA TCC TGT GTG CCC
40 P D E I E Y I F K P S C V P
+40 +45 +50

CTG ATG CGA TGC GGG GGC TGC TGC AAT GAC GAG GGC CTG
L M R C G G C C N D E G L
+55 +60 +65

333 GAG TGT GTG CCC ACT GAG GAG TCC AAC ATC ACC ATG CAG ATT
67 E C V P T E E S N I T M Q I
+70 +75 +80

ATG CGG ATC AAA CCT CAC CAA GGC CAG CAC ATA GGA GAG
M R I K P H Q G Q H I G E
+85 +90

414 ATG AGC TTC CTA CAG CAC AAC AAA TGT GAA TGC AGA CCA AAG
94 M S F L Q H N K C E C R P K
+95 +100 +105

AAA GAT AGA GCA AGA CAA GAA AAT CCC TGT GGG CCT TGC
K D R A R Q E N P C G P C
+110 +115 +120

495 TCA GAG CGG AGA AAG CAT TTG TTT GIA CAA GAT CCG CAG ACC
121 S E R R K H L F V Q D P Q T
+125 +130

TGT AAA TGT TCC TGC AAA AAC ACA GAC TCG CGT TGC AAG
C K C S C K N T D S R C K
+135 +140 +145

FIG. 1A

576 GCG AGG CAG CTT GAG TTA AAC GAA CGT ACT TGC AGA TGT GAC
148 A R Q L E L N E R T C R C D
+150 +155 +160

AAG CCG AGG CGG TGA GCCGGGCA GGAGGAAGGA GCCTCCCTCA
K P R R O
+165

661 GGGTTTCGGG ACCAGATCT CTCACCAGGA AAGACTGATA CAGAACGATC
GATACAGAAA CCACGCTGCC GCCACCACAC CATCACCATC GACAGAACAG

761 TCCTTAATCC AGAAACCTGA AATGAAGGAA GAGGAGACTC TGCGCAGAGC
ACTTTGGGTC CGGAGGGCGA GACTCCGGCG GAAGCATTCC CGGGCGGGTG

861 ACCCAGCACG GTCCCTTTG GAATGGATT CGCCATTTA TTTTCTTGC
TGCTAAATCA CCGAGCCCCGG AAGATTAGAG AGTTTATTT CTGGGATTCC

961 TGTAGACACA CGCGGGCCGC CAGCACACTG

FIG. 1B

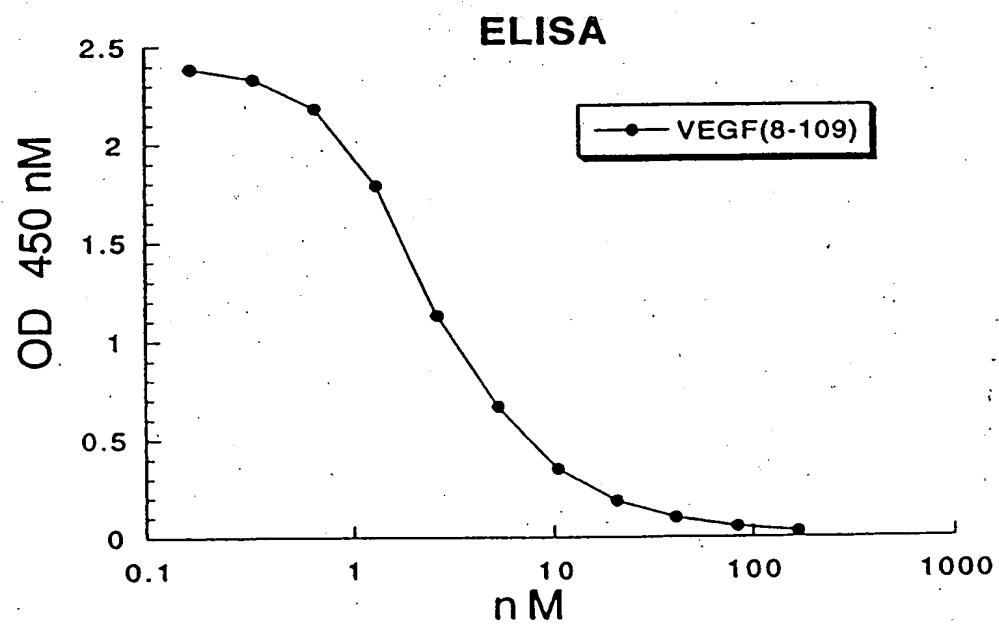


Fig. 2

KIRA

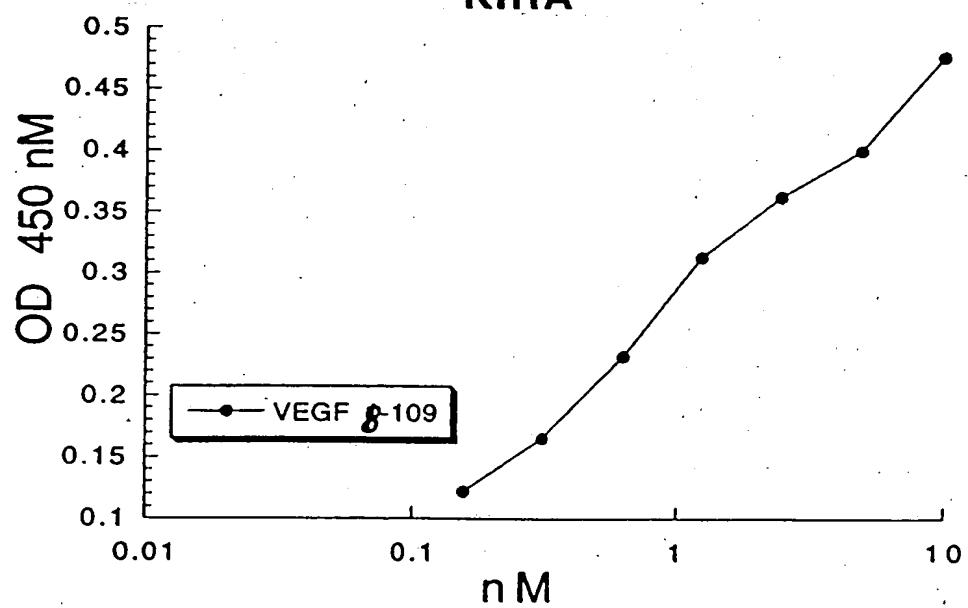


Fig. 3

0000000000000000

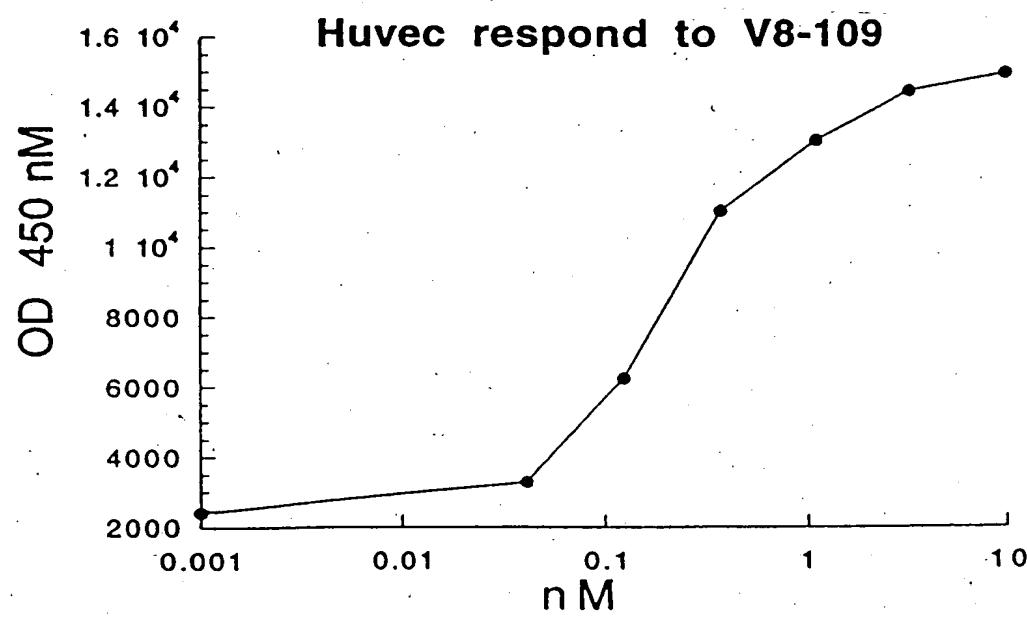


Fig. 4

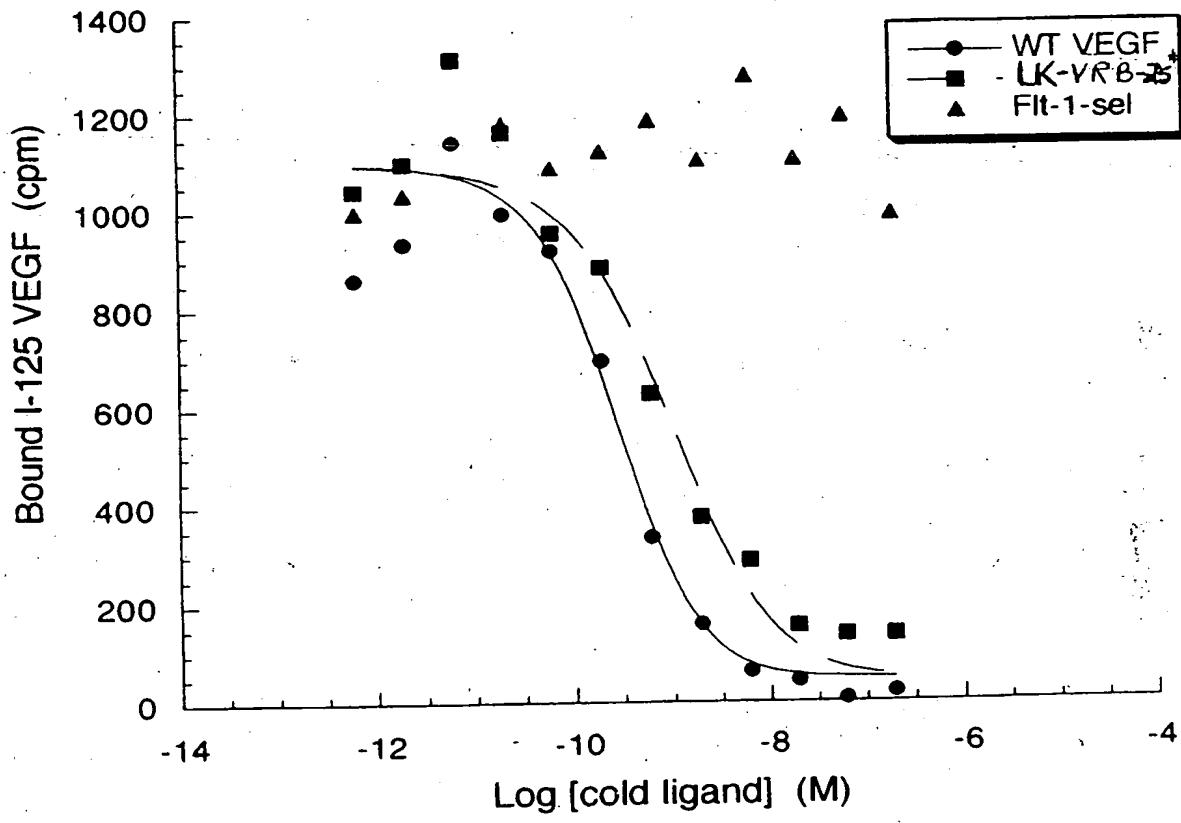


Fig. 5

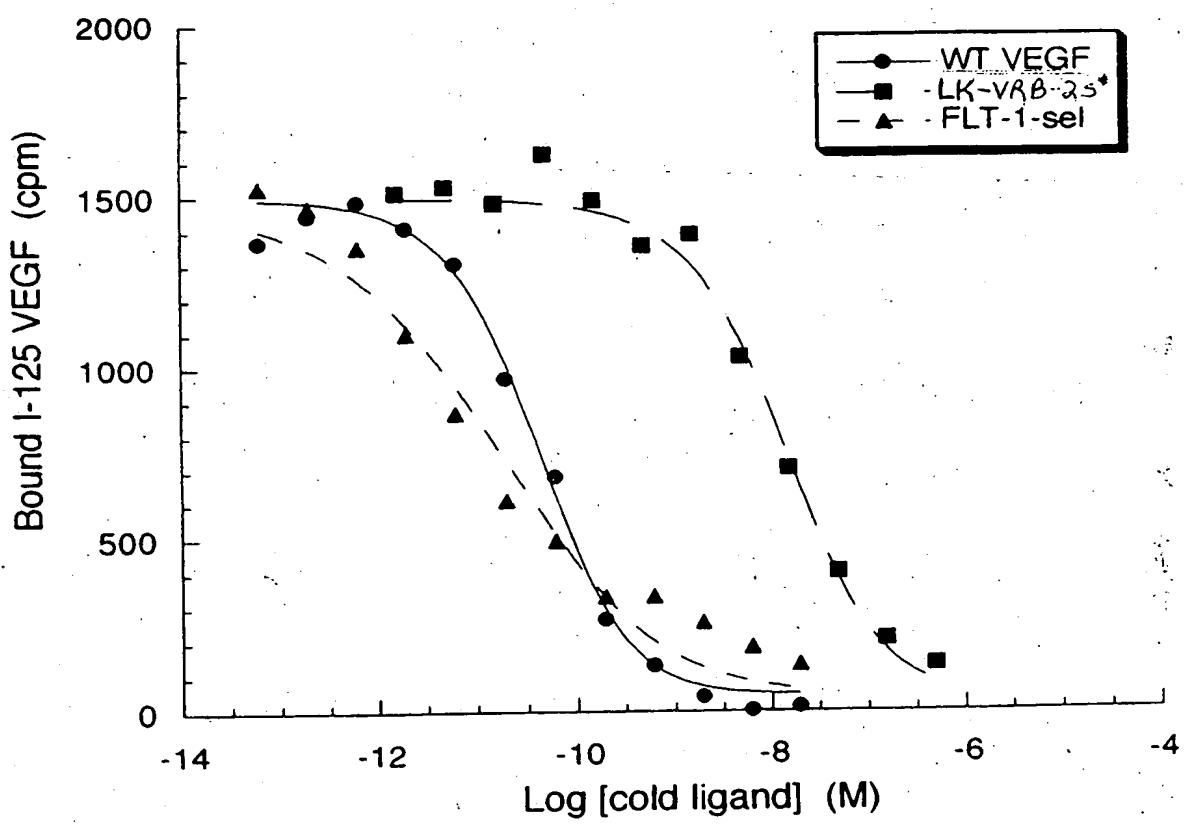


Fig. 6

Fold reduction in binding of VEGF alanine mutants

Residue	KDR(1-3)	Flt(1-3)
VEGF(1-109)	1 (10 nM)	1 (6 nM)
20s helix:		
Lys 16	1	1
Phe 17*	45	34
Met 18**	5	9
Tyr 21**	19	29
Gln 22**	6	15
Tyr 25**	6	7
40s loop:		
Ile 43*	21	3
Ile 46*	96	4
Phe 47**	5	3
Lys 48**	1	1
60s loop:		
Asp 63**	1	8
Glu 64*	10	5
Gly 65**	1	1
Leu 66**	1	10
80s loop:		
Gln 79*	55	3
Met 81**	9	5
Ile 83*	89	7
His 86**	2	1
Gln 89	1	1
Ile 91	1	1
100s loop:		
Lys 101	1	1
Glu 103	1	1
Arg 105	1	1
Pro 106	1	1

Fig. 7

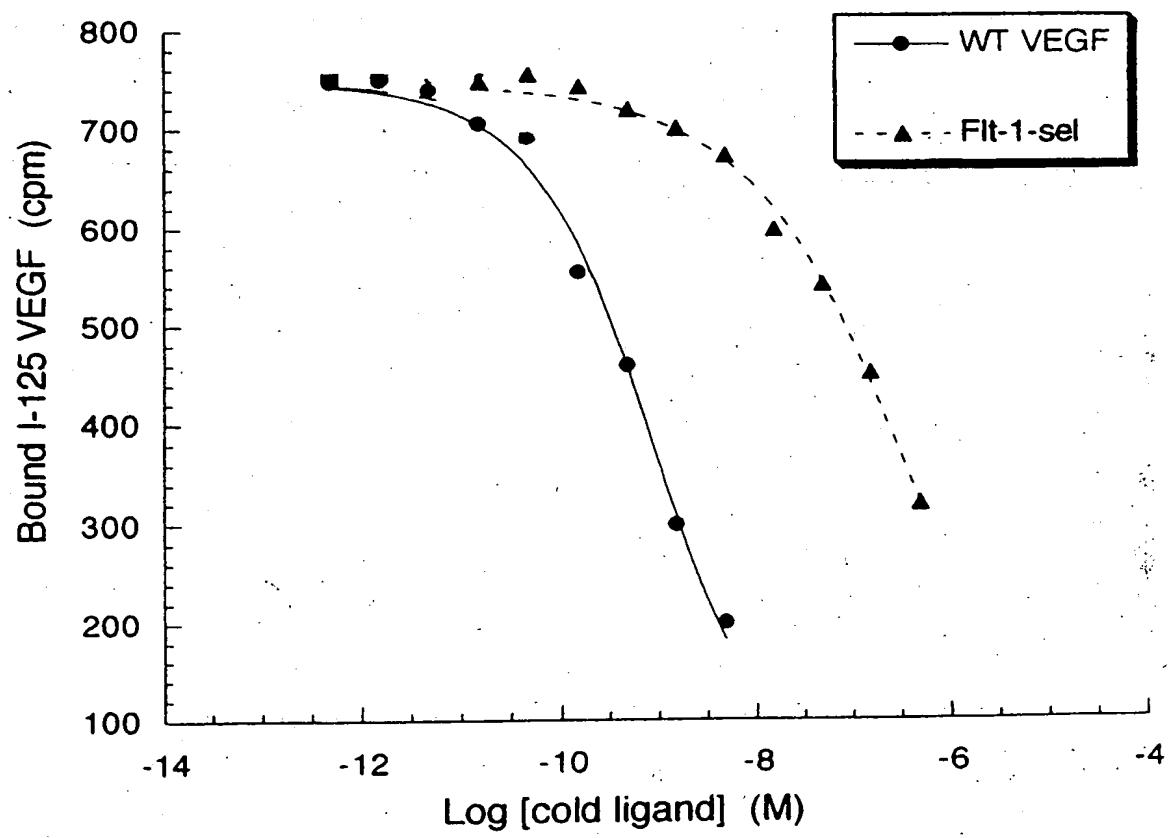


Fig. 8A

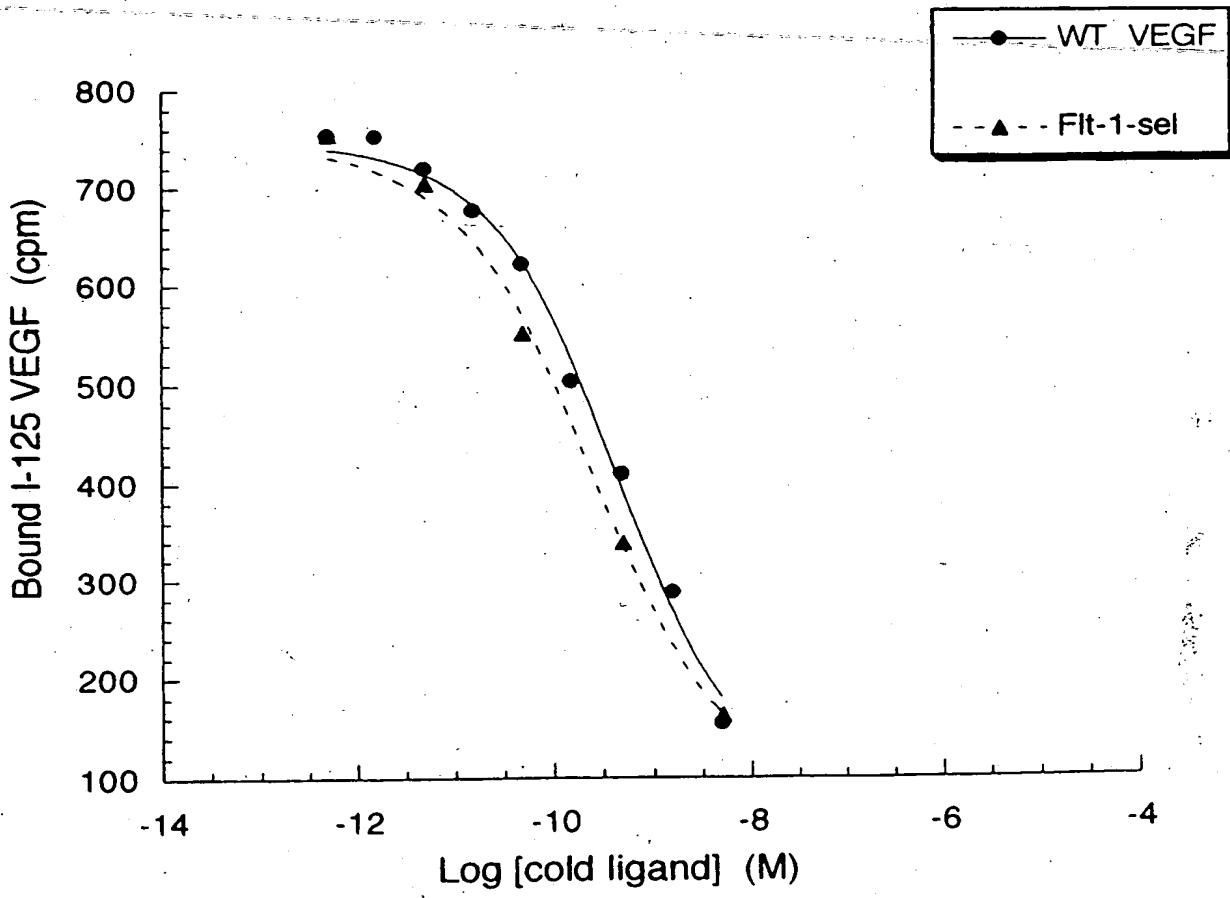


Fig. 8B

ODD THERAPY EXPRESSION

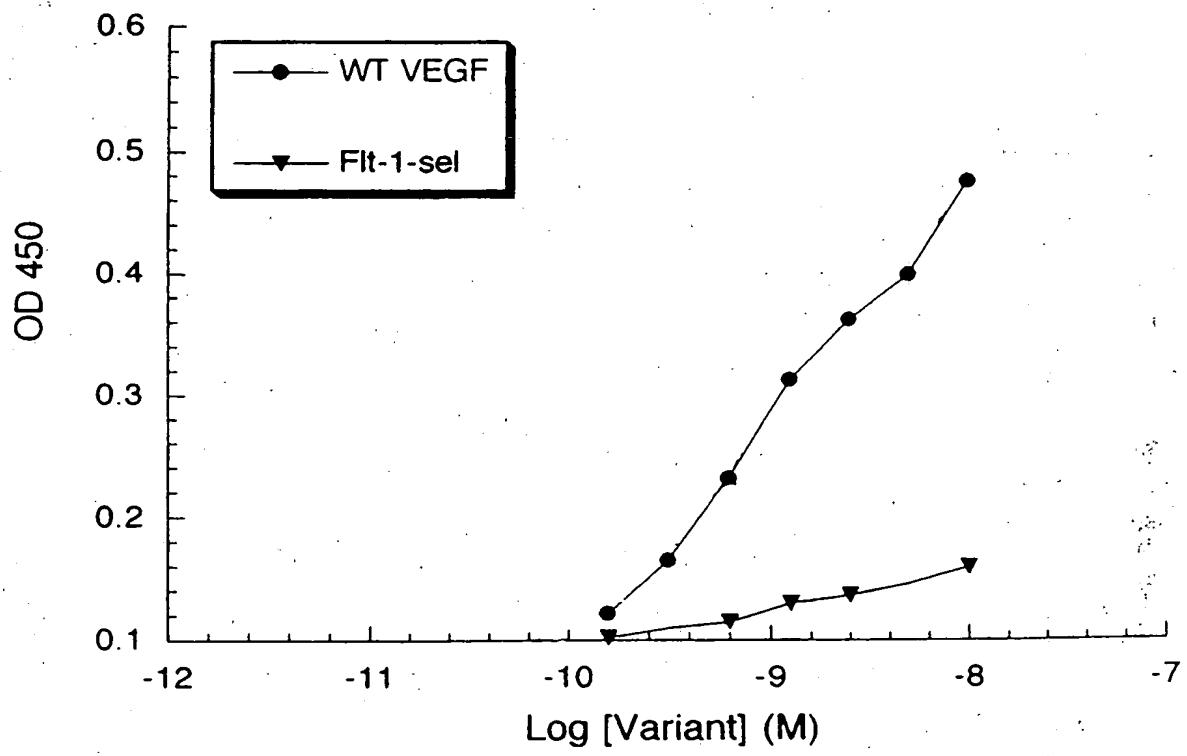


Fig. 9

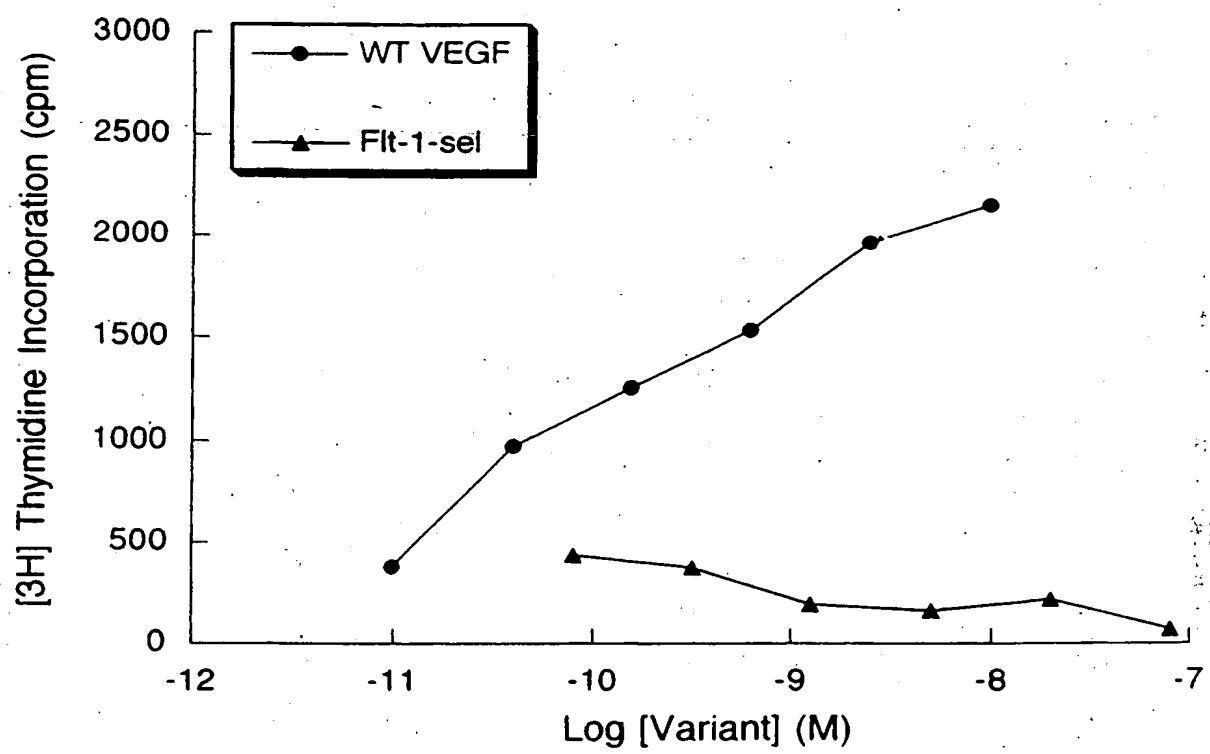


Fig. 10

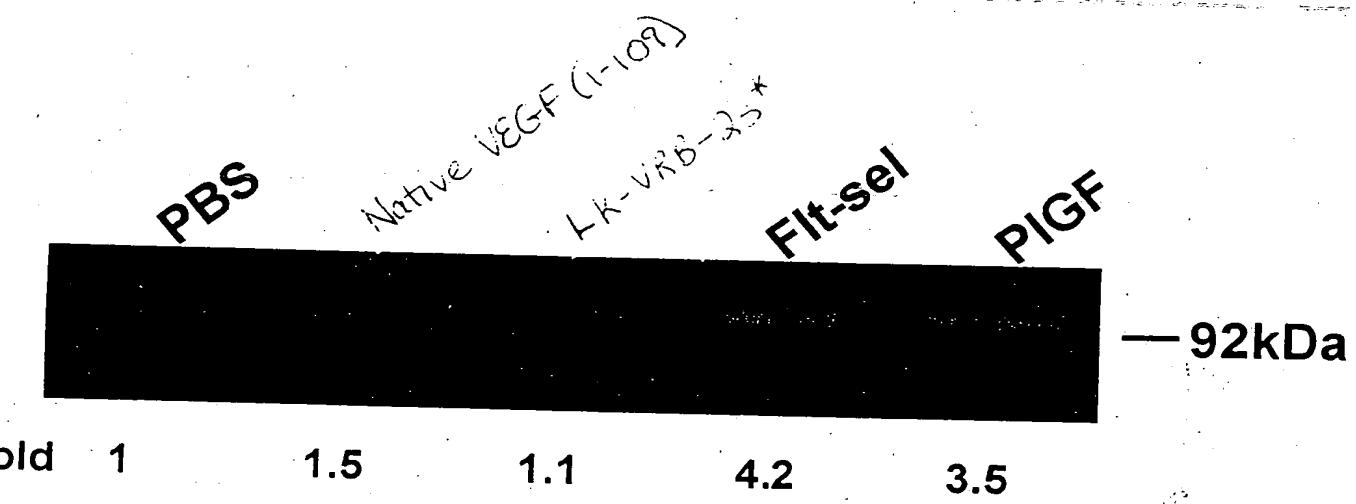


Fig. 11

Figure 12A

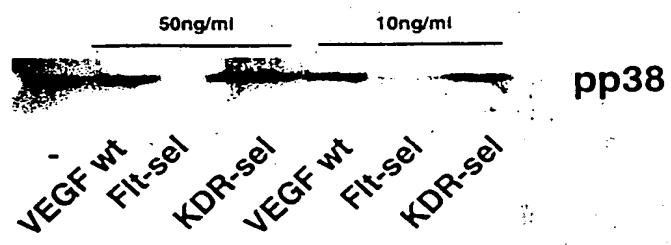


50ng/ml 10ng/ml

ppERK 1
ppERK 2

VEGF WT Fit-sel KDR-sel VEGF WT Fit-sel KDR-sel

Fig. 12B



50ng/ml 10ng/ml

pp38

VEGF WT Fit-sel KDR-sel VEGF WT Fit-sel KDR-sel

Fig
13A

IP: α -PLC γ 1
ECL: α -pTyr

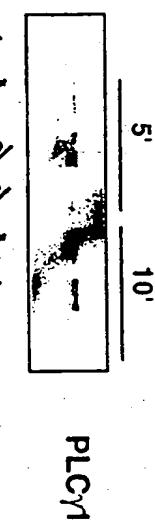
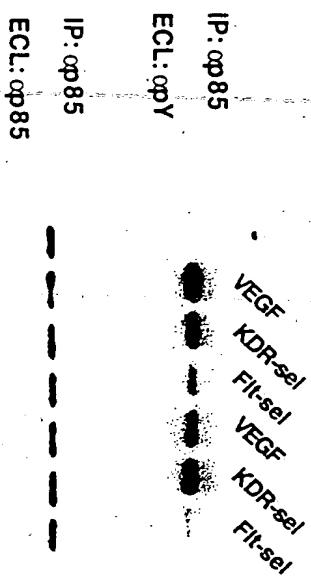


Fig
13B



00545857 041000

Fig.
14A

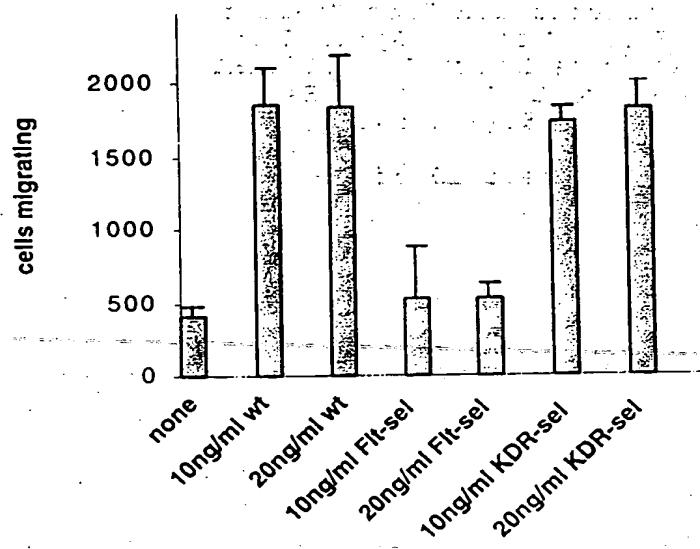


Fig.
14B

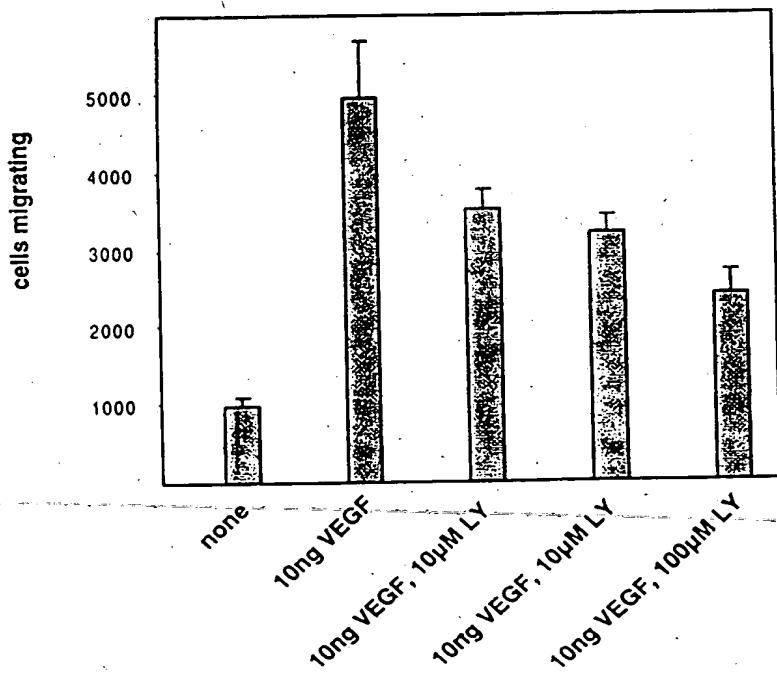
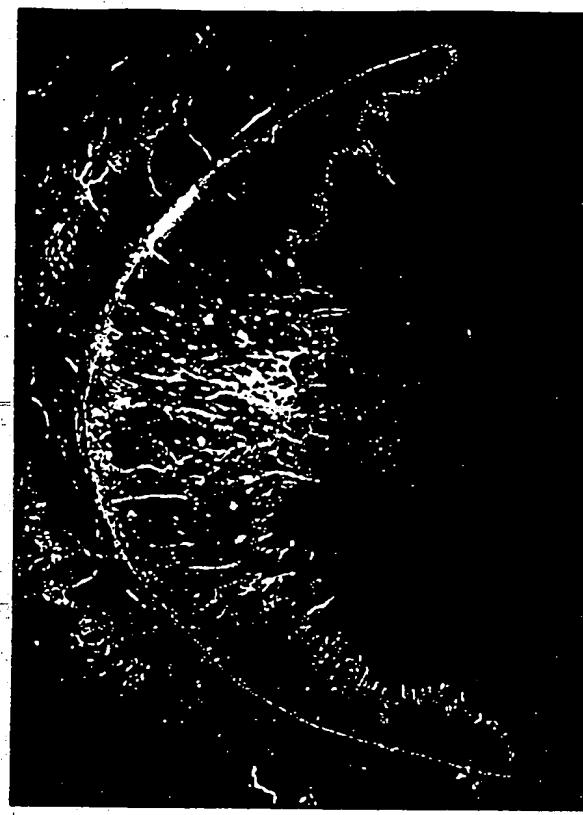
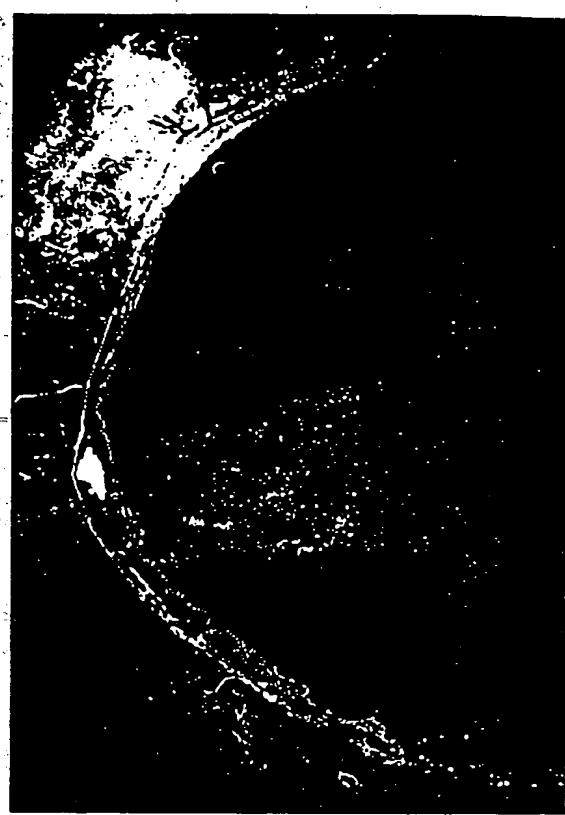


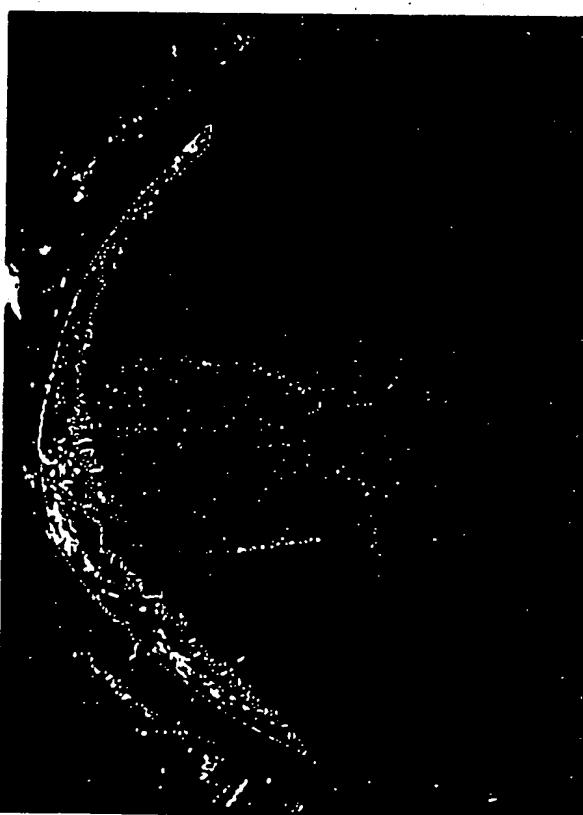
Fig. 15A



KDR-selective VEGF



Control



Flt-selective VEGF



VEGF

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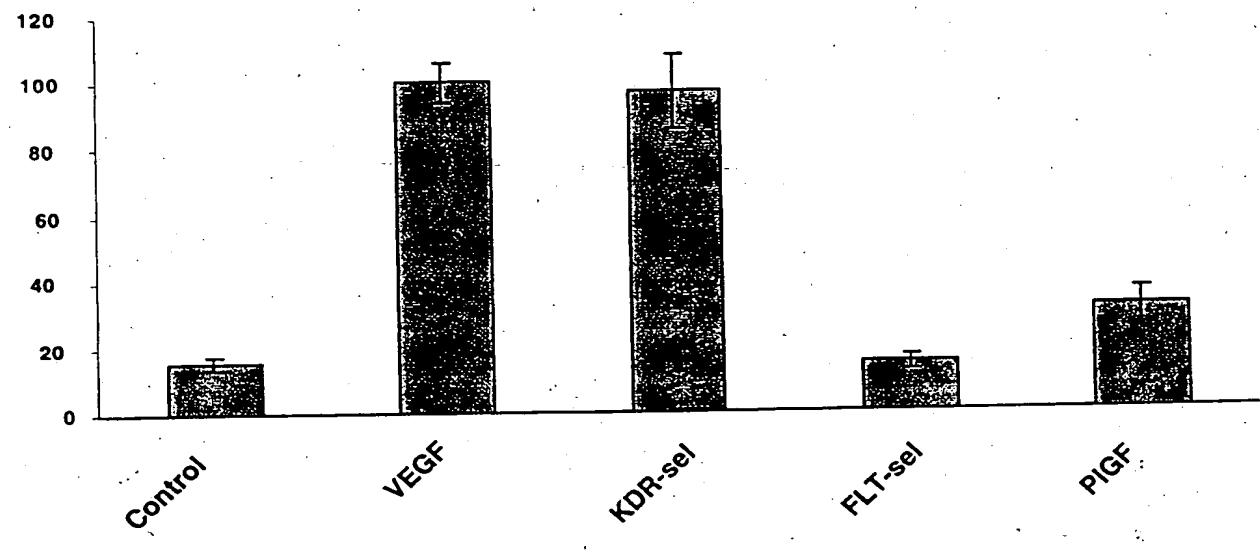


Fig. 15B